



SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Lonsdale, John
Milner, Peter
Payne, David
Pearson, Stewart

(ii) TITLE OF THE INVENTION: Novel FabI

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SmithKline Beecham Corporation
(B) STREET: 709 Swedeland Road
(C) CITY: King of Prussia
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19406-0939

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 28-August-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/024845
(B) FILING DATE: 28-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Gimmi, Edward R
(B) REGISTRATION NUMBER: 38,891
(C) REFERENCE/DOCKET NUMBER: GM50005

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 610-270-4478

(B) TELEFAX: 610-270-5090

(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Leu	Asn	Leu	Glu	Asn	Lys	Thr	Tyr	Val	Ile	Met	Gly	Ile	Ala	Asn
1				5					10						15
Lys	Arg	Ser	Ile	Ala	Phe	Gly	Val	Ala	Lys	Val	Leu	Asp	Gln	Leu	Gly
					20				25						30
Ala	Lys	Leu	Val	Phe	Thr	Tyr	Arg	Lys	Glu	Arg	Ser	Arg	Lys	Glu	Leu
					35			40							45
Glu	Lys	Leu	Leu	Glu	Gln	Leu	Asn	Gln	Pro	Glu	Ala	His	Leu	Tyr	Gln
					50			55							60
Ile	Asp	Val	Gln	Ser	Asp	Glu	Glu	Val	Ile	Asn	Gly	Phe	Glu	Gln	Ile
					65			70							80
Gly	Lys	Asp	Val	Gly	Asn	Ile	Asp	Gly	Val	Tyr	His	Ser	Ile	Ala	Phe
					85			90							95
Ala	Asn	Met	Glu	Asp	Leu	Arg	Gly	Arg	Phe	Ser	Glu	Thr	Ser	Arg	Glu
					100			105							110
Gly	Phe	Leu	Leu	Ala	Gln	Asp	Ile	Ser	Ser	Tyr	Ser	Leu	Thr	Ile	Val
					115			120							125
Ala	His	Glu	Ala	Lys	Lys	Leu	Met	Pro	Glu	Gly	Gly	Ser	Ile	Val	Ala
					130			135							140
Thr	Thr	Tyr	Leu	Gly	Gly	Glu	Phe	Ala	Val	Gln	Asn	Tyr	Asn	Val	Met
					145			150				155			160
Gly	Val	Ala	Lys	Ala	Ser	Leu	Glu	Ala	Asn	Val	Lys	Tyr	Leu	Ala	Leu
					165			170							175
Asp	Leu	Gly	Pro	Asp	Asn	Ile	Arg	Val	Asn	Ala	Ile	Ser	Ala	Gly	Pro
					180			185							190
Ile	Arg	Thr	Leu	Ser	Ala	Lys	Gly	Val	Gly	Gly	Phe	Asn	Thr	Ile	Leu
					195			200							205
Lys	Glu	Ile	Glu	Glu	Arg	Ala	Pro	Leu	Lys	Arg	Asn	Val	Asp	Gln	Val
					210			215							220

Glu	Val	Gly	Lys	Thr	Ala	Ala	Tyr	Leu	Leu	Ser	Asp	Leu	Ser	Ser	Gly
225							230			235					240
Val	Thr	Gly	Glu	Asn	Ile	His	Val	Asp	Ser	Gly	Phe	His	Ala	Ile	Lys
					245			250						255	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGTTAAATC	TTGAAAACAA	AACATATGTC	ATCATGGAA	TCGCTAATAA	GCGTAGTATT	60
GCTTTTGGTG	TCGCTAAAGT	TTTAGATCAA	TTAGGTGCTA	AATTAGTATT	TACTTACCGT	120
AAAGAACGTA	GCCGTAAGA	GCTTGAAAAA	TTATTAGAAC	AATTAAATCA	ACCAGAACGCG	180
CACTTATATC	AAATTGATGT	TCAAAGCGAT	GAAGAGGTTA	TTAATGGTTT	TGAGCAAATT	240
GGTAAAGATG	TTGCAATAT	TGATGGTGTA	TATCATTCAA	TCGCATTG	TAATATGGAA	300
GACTTACCGCG	GACGCTTTC	TGAAACTTCA	CGTGAAGGCT	TCTTGTAGC	TCAAGACATT	360
AGTTCTTACT	CATTAACAAT	TGTGGCTCAT	GAAGCTAAAA	AATTAAATGCC	AGAAGGTGGT	420
AGCATTGTTG	CAACAAACATA	TTTAGGTGGC	GAATTCGCAG	TTCAAAATTA	TAATGTGATG	480
GGTGGTGCTA	AAGCGAGCTT	AGAAGCAAAT	GTTAAATATT	TAGCATTAGA	CTTAGGTCCCT	540
GATAATATTC	GCGTTAATGC	AATTCAGCT	GGTCCAATCC	GTACATTAAG	TGCAAAAGGT	600
GTGGGTGGTT	TCAATACAAT	TCTTAAAGAA	ATCGAAGAGC	GTGCACCTTT	AAAACGTAAC	660
GTTGATCAAG	TAGAAGTAGG	TAAAACAGCG	GCTTACTTRT	TAAGTGACTT	ATCAAGTGCG	720
GTTACAGGTG	AAAATATTCA	TGTAGATAGC	GGATTCCACG	CAATTAAATA	A	771